

Patent Application US/07/946,236

SEQUENCE LISTING

OK

(1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Cindy A.
Smith, Craig A.

(ii) TITLE OF INVENTION: Method of Treating TNF-Dependent
Inflammation Using Tumor Necrosis Factor Antagonists

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: U.S.A.
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wight, Christopher L.
(B) REGISTRATION NUMBER: 31,680
(C) REFERENCE/DOCKET NUMBER: 2503

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 587-0606

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

Patent Application US/07/946,236

54
55 (iv) ANTI-SENSE: NO
56
57 (vi) ORIGINAL SOURCE:
58 (A) ORGANISM: Homo sapiens
59 (G) CELL TYPE: Fibroblast
60 (H) CELL LINE: WI-26 VA4
61
62 (vii) IMMEDIATE SOURCE:
63 (A) LIBRARY: WI-26 VA4
64 (B) CLONE: Clone 1
65
66 (ix) FEATURE:
67 (A) NAME/KEY: CDS
68 (B) LOCATION: 88..1473
69
70 (ix) FEATURE:
71 (A) NAME/KEY: mat_peptide
72 (B) LOCATION: 154..1470
73
74 (ix) FEATURE:
75 (A) NAME/KEY: sig_peptide
76 (B) LOCATION: 88..153
77
78
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
80
81 GCGAGGCAGG CAGCCTGGAG AGAAGGCGCT GGGCTGCGAG GCGCGGAGGG CGCGAGGGCA 6
82
83 GGGGGCAACC GGACCCCGCC CGCATCC ATG GCG CCC GTC GCC GTC TGG GCC 11
84 Met Ala Pro Val Ala Val Trp Ala
85 -22 -20 -15
86
87 GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC 15
88 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
89 -10 -5 1
90
91 GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC 20
92 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
93 5 10 15
94
95 CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA 25
96 Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
97 20 25 30
98
99 TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC 30
100 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
101 35 40 45 50
102
103 ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC 35
104 Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
105 55 60 65
106

Patent Application US/07/946,236

107	TGG	GTT	CCC	GAG	TGC	TTG	AGC	TGT	GGC	TCC	CGC	TGT	AGC	TCT	GAC	CAG	39
108	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	
109				70					75					80			
110																	
111	GTG	GAA	ACT	CAA	GCC	TGC	ACT	CGG	GAA	CAG	AAC	CGC	ATC	TGC	ACC	TGC	44
112	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys	
113			85					90					95				
114																	
115	AGG	CCC	GGC	TGG	TAC	TGC	GCG	CTG	AGC	AAG	CAG	GAG	GGG	TGC	CGG	CTG	49
116	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	
117		100					105					110					
118																	
119	TGC	GCG	CCG	CTG	CGC	AAG	TGC	CGC	CCG	GGC	TTC	GGC	GTG	GCC	AGA	CCA	54
120	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	
121	115					120					125					130	
122																	
123	GGA	ACT	GAA	ACA	TCA	GAC	GTG	GTG	TGC	AAG	CCC	TGT	GCC	CCG	GGG	ACG	59
124	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	
125					135					140					145		
126																	
127	TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG	CCC	CAC	CAG	ATC	63
128	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
129				150					155					160			
130																	
131	TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	68
132	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	
133			165					170					175				
134																	
135	ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	73
136	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
137		180					185					190					
138																	
139	CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	78
140	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
141	195					200					205					210	
142																	
143	CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	83
144	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
145					215					220				225			
146																	
147	CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	87
148	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
149				230					235					240			
150																	
151	ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	92
152	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
153			245					250					255				
154																	
155	TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	97
156	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
157		260					265					270					
158																	
159	GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG	102

160	Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	
161	275					280					285					290	
162																	
163	GGC	CCC	GAG	CAG	CAG	CAC	CTG	CTG	ATC	ACA	GCG	CCG	AGC	TCC	AGC	AGC	107
164	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	
165					295					300					305		
166																	
167	AGC	TCC	CTG	GAG	AGC	TCG	GCC	AGT	GCG	TTG	GAC	AGA	AGG	GCG	CCC	ACT	111
168	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	
169				310					315					320			
170																	
171	CGG	AAC	CAG	CCA	CAG	GCA	CCA	GGC	GTG	GAG	GCC	AGT	GGG	GCC	GGG	GAG	116
172	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	
173			325					330					335				
174																	
175	GCC	CGG	GCC	AGC	ACC	GGG	AGC	TCA	GAT	TCT	TCC	CCT	GGT	GGC	CAT	GGG	121
176	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	
177		340					345					350					
178																	
179	ACC	CAG	GTC	AAT	GTC	ACC	TGC	ATC	GTG	AAC	GTC	TGT	AGC	AGC	TCT	GAC	126
180	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	
181	355					360					365					370	
182																	
183	CAC	AGC	TCA	CAG	TGC	TCC	TCC	CAA	GCC	AGC	TCC	ACA	ATG	GGA	GAC	ACA	131
184	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	
185					375					380					385		
186																	
187	GAT	TCC	AGC	CCC	TCG	GAG	TCC	CCG	AAG	GAC	GAG	CAG	GTC	CCC	TTC	TCC	135
188	Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	
189				390					395					400			
190																	
191	AAG	GAG	GAA	TGT	GCC	TTT	CGG	TCA	CAG	CTG	GAG	ACG	CCA	GAG	ACC	CTG	140
192	Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser	Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu	
193			405					410					415				
194																	
195	CTG	GGG	AGC	ACC	GAA	GAG	AAG	CCC	CTG	CCC	CTT	GGA	GTG	CCT	GAT	GCT	145
196	Leu	Gly	Ser	Thr	Glu	Glu	Lys	Pro	Leu	Pro	Leu	Gly	Val	Pro	Asp	Ala	
197		420					425					430					
198																	
199	GGG	ATG	AAG	CCC</													

Patent Application US/07/946,236

213 (A) LENGTH: 461 amino acids
 214 (B) TYPE: amino acid
 215 (D) TOPOLOGY: linear
 216
 217 (ii) MOLECULE TYPE: protein
 218
 219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 220
 221 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 222 -22 -20 -15 -10
 223
 224 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 225 -5 1 5 10
 226
 227 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 228 15 20 25
 229
 230 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 231 30 35 40
 232
 233 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 234 45 50 55
 235
 236 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 237 60 65 70
 238
 239 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 240 75 80 85 90
 241
 242 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 243 95 100 105
 244
 245 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 246 110 115 120
 247
 248 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 249 125 130 135
 250
 251 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 252 140 145 150
 253
 254 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 255 155 160 165 170
 256
 257 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 258 175 180 185
 259
 260 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 261 190 195 200
 262
 263 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 264 205 210 215
 265

Patent Application US/07/946,236

266 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
267 220 225 230
268
269 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
270 235 240 245 250
271
272 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
273 255 260 265
274
275 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
276 270 275 280
277
278 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
279 285 290 295
280
281 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
282 300 305 310
283
284 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
285 315 320 325 330
286
287 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
288 335 340 345
289
290 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
291 350 355 360
292
293 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
294 365 370 375
295
296 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
297 380 385 390
298
299 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
300 395 400 405 410
301
302 Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
303 415 420 425
304
305 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
306 430 435
307
308

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

Patent Application US/07/946,236

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319      (iii) HYPOTHETICAL: NO
320
321      (iv) ANTI-SENSE: NO
322
323
324      (vii) IMMEDIATE SOURCE:
325            (B) CLONE: TNFR/Fc Fusion Protein
326
327      (ix) FEATURE:
328            (A) NAME/KEY: CDS
329            (B) LOCATION: 1..1557
330
331      (ix) FEATURE:
332            (A) NAME/KEY: mat_peptide
333            (B) LOCATION: 1..1554
334
335
336      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
337
338      GCG AGG CAG GCA GCC TGG AGA GAA GGC GCT GGG CTG CGA GGG CGC GAG      4
339      Ala Arg Gln Ala Ala Trp Arg Glu Gly Ala Gly Leu Arg Gly Arg Glu
340      1              5              10              15
341
342      GGC GCG AGG GCA GGG GGC AAC CGG ACC CCG CCC GCA TCC ATG GCG CCC      9
343      Gly Ala Arg Ala Gly Gly Asn Arg Thr Pro Pro Ala Ser Met Ala Pro
344      20              25              30
345
346      GTC GCC GTC TGG GCC GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG      14
347      Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
348      35              40              45
349
350      GCG CAC GCC TTG CCC GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG      19
351      Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu
352      50              55              60
353
354      CCC GGG AGC ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG      24
355      Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln
356      65              70              75              80
357
358      ATG TGC TGC AGC AAA TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT      28
359      Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys
360      85              90              95
361
362      ACC AAG ACC TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC      33
363      Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr
364      100              105              110
365
366      ACC CAG CTC TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC      38
367      Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg
368      115              120              125
369
370      TGT AGC TCT GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC      43
371      Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn

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Patent Application US/07/946,236

	130	135	140	
372				
373				
374	CGC ATC TGC ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG			48
375	Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln			
376	145	150	155	160
377				
378	GAG GGG TGC CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC			52
379	Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe			
380		165	170	175
381				
382	GGC GTG GCC AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC			57
383	Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro			
384		180	185	190
385				
386	TGT GCC CCG GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC			62
387	Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys			
388		195	200	205
389				
390	AGG CCC CAC CAG ATC TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC			67
391	Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser			
392		210	215	220
393				
394	ATG GAT GCA GTC TGC ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA			72
395	Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro			
396		225	230	235
397				
398	GGG GCA GTA CAC TTA CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG			76
399	Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr			
400		245	250	255
401				
402	CAG CCA ACT CCA GAA CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC			81
403	Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu			
404		260	265	270
405				
406	CCA ATG GGC CCC AGC CCC CCA GCT GAA GGG AGC ACT GGC GAC GAG CCC			86
407	Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Glu Pro			
408		275	280	285
409				
410	AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA			91
411	Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			
412		290	295	300
413				
414	CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC			96
415	Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			
416		305	310	315
417				
418	ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC			100
419	Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			
420		325	330	335
421				
422	GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC			105
423	Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
424		340	345	350

Patent Application US/07/946,236

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425
426 GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC      110
427 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
428           355                      360                      365
429
430 AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG      115
431 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
432           370                      375                      380
433
434 CTG AAT GGC AAG GAC TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA      120
435 Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
436 385                      390                      395                      400
437
438 GCC CCC ATG CAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA      124
439 Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
440           405                      410                      415
441
442 CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC      129
443 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
444           420                      425                      430
445
446 CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGG CAC ATC      134
447 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile
448           435                      440                      445
449
450 GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC      139
451 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
452 450                      455                      460
453
454 ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG      144
455 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
456 465                      470                      475                      480
457
458 CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC      148
459 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
460           485                      490                      495
461
462 TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC      153
463 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
464           500                      505                      510
465
466 TCC CTG TCT CCG GGT AAA TGA      15
467 Ser Leu Ser Pro Gly Lys
468 515
469
470
471 (2) INFORMATION FOR SEQ ID NO:4:
472
473 (i) SEQUENCE CHARACTERISTICS:
474 (A) LENGTH: 518 amino acids
475 (B) TYPE: amino acid
476 (D) TOPOLOGY: linear
477

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Patent Application US/07/946,236

478 (ii) MOLECULE TYPE: protein

479

480 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

481

482 Ala Arg Gln Ala Ala Trp Arg Glu Gly Ala Gly Leu Arg Gly Arg Glu

483 1 5 10 15

484

485 Gly Ala Arg Ala Gly Gly Asn Arg Thr Pro Pro Ala Ser Met Ala Pro

486 20 25 30

487

488 Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala

489 35 40 45

490

491 Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu

492 50 55 60

493

494 Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln

495 65 70 75 80

496

497 Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys

498 85 90 95

499

500 Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr

501 100 105 110

502

503 Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg

504 115 120 125

505

506 Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn

507 130 135 140

508

509 Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln

510 145 150 155 160

511

512 Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe

513 165 170 175

514

515 Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro

516 180 185 190

517

518 Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys

519 195 200 205

520

521 Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser

522 210 215 220

523

524 Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro

525 225 230 235 240

526

527 Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr

528 245 250 255

529

530 Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu

531				260				265				270					
532																	
533	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Glu	Pro	
534			275					280					285				
535																	
536	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
537		290					295					300					
538																	
539	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
540	305					310					315					320	
541																	
542	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
543					325					330					335		
544																	
545	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
546				340					345					350			
547																	
548	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	
549			355					360					365				
550																	
551	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	
552		370					375					380					
553																	
554	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	
555	385					390					395					400	
556																	
557	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	
558					405					410					415		
559																	
560	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	
561				420					425					430			
562																	
563	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	His	Ile	
564			435					440					445				
565																	
566	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	
567		450					455					460					
568																	
569	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	
570	465					470					475					480	
571																	
572	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	
573					485					490					495		
57																	

(2) INFORMATION FOR SEQ ID NO:5:

Patent Application US/07/946,236

584 (i) SEQUENCE CHARACTERISTICS:
585 (A) LENGTH: 22 base pairs
586 (B) TYPE: nucleic acid
587 (C) STRANDEDNESS: single
588 (D) TOPOLOGY: linear
589
590 (ii) MOLECULE TYPE: DNA (genomic)
591
592 (iii) HYPOTHETICAL: NO
593
594 (iv) ANTI-SENSE: YES
595
596
597 (vii) IMMEDIATE SOURCE:
598 (B) CLONE: oligonucleotide
599
600
601 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
602
603 CGGTACGTGC TGTGTTACT GC

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/946,236

DATE: 09/26/92
TIME: 12:25:19

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SEQUENCE MISSING ITEM REPORT
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PRIOR APPLICATION DATA
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